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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Fri Aug 03 11:07:58 EDT 2007

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\*\*\*\*\*

Reviewer Comments:

10583785 errors

<210> 6

<211> 1671

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1) ... (837)

<223> Coding sequence of human SP-B precursor lacking the C-terminal propeptide

<220>

<221> CDS

<222> (844) ... (1671)

<223> Coding sequence of low mw two-chain urokinase-plasminogen activator

What about locations 838 through 843? They are not explained. This type of error also appears in Sequences 7, 12, 13, 19, 20, 25, and 26. See below for another error in Sequence 19.

<210> 19

<211> 557

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1) ... (279)

<223> Human surfactant protein B precursor lacking the C-terminal  
propeptide

<220>

<221> PEPTIDE

<222> (282) ... (577)

<223> Human low molecular weight two-chain urokinase-plasminogen  
activator

Not only are locations 280 through 281 not explained, but the above  
<222> response is incorrect. It states <222> (282) ... (577); however,  
only 557 amino acids are in the sequence.

<400> 26

Met	Arg	Ala	Leu	Leu	Ala	Arg	Leu	Leu	Leu	Cys	Val	Leu	Val	Val	Ser
1				5					10					15	

Asp	Ser	Lys	Gly	Ser	Asn	Lys	Pro	Ser	Ser	Pro	Pro	Glu	Glu	Leu	Lys
				20					25					30	

Please delete the blank line between the above amino acids and their  
numbering.

\*\*\*\*\*

Application No: 10583785

Version No: 3.0

**Input Set:****Output Set:**

**Started:** 2007-07-24 12:08:44.453  
**Finished:** 2007-07-24 12:08:47.371  
**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 918 ms  
**Total Warnings:** 8  
**Total Errors:** 10  
**No. of SeqIDs Defined:** 26  
**Actual SeqID Count:** 26

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (26)

**Input Set:**

**Output Set:**

**Started:** 2007-07-24 12:08:44.453  
**Finished:** 2007-07-24 12:08:47.371  
**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 918 ms  
**Total Warnings:** 8  
**Total Errors:** 10  
**No. of SeqIDs Defined:** 26  
**Actual SeqID Count:** 26

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (26)

# SEQUENCE LISTING

<110> Werner Seeger

<120> Novel Chimeric Plasminogen Activators and Their Pharmaceutical Use

<130> 607927-000001

<140> 10583785

<141> 2007-07-24

<150> US/10/583,785

<151> 2006-06-19

<160> 26

<210> 1

<211> 1143

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (1143)

<223> Coding sequence of the surfactant protein B precursor

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Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr	
1 5 10 15	

ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt	96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys	
20 25 30	

gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag	144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln	
35 40 45	

tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga	192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	
50 55 60	

gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac	240
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn	
65 70 75 80	

aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg	288
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu	
85 90 95	

gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc	336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	
100 105 110	

aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag	384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	
115 120 125	

aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa	432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	
130 135 140	
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg	480
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu	
145 150 155 160	
ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc	528
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu	
165 170 175	
gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac	576
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His	
180 185 190	
aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc	624
Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys	
195 200 205	
tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag	672
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys	
210 215 220	
ggg ggc cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg	720
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu	
225 230 235 240	
gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc	768
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile	
245 250 255	
ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc	816
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg	
260 265 270	
ctc gtc ctc cgg tgc tcc atg gat gac agc gct ggc cca agg tcg ccg	864
Leu Val Leu Arg Cys Ser Met Asp Asp Ser Ala Gly Pro Arg Ser Pro	
275 280 285	
aca gga gaa tgg ctg ccg cga gac tct gag tgc cac ctc tgc atg tcc	912
Thr Gly Glu Trp Leu Pro Arg Asp Ser Glu Cys His Leu Cys Met Ser	
290 295 300	
gtg acc acc cag gcc ggg aac agc agc gag cag gcc ata cca cag gca	960
Val Thr Thr Gln Ala Gly Asn Ser Ser Glu Gln Ala Ile Pro Gln Ala	
305 310 315 320	
atg ctc cag gcc tgt gtt ggc tcc tgg ctg gac agg gaa aag tgc aag	1008
Met Leu Gln Ala Cys Val Gly Ser Trp Leu Asp Arg Glu Lys Cys Lys	
325 330 335	
caa ttt gtg gag cag cac acg ccc cag ctg ctg acc ctg gtg ccc agg	1056
Gln Phe Val Glu Gln His Thr Pro Gln Leu Leu Thr Leu Val Pro Arg	
340 345 350	

ggc tgg gat gcc cac acc acc tgc cag gcc ctc ggg gtg tgt ggg acc 1104  
Gly Trp Asp Ala His Thr Thr Cys Gln Ala Leu Gly Val Cys Gly Thr  
355 360 365

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<210> 2
<211> 837
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) ... (837)
<223> Coding sequence of SP-B precursor lacking the C-terminal propeptide

<400> 2
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ctc tgt gcc cca gcc act gct gcc tgg acc acc tca tcc ttg gcc tgt 96  
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys  
20 25 30

tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga 192  
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly  
50 55 60

aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg 288  
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu  
85 90 95

aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag 384  
 Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln  
 115 120 125

tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg 480  
 Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu  
 145 150 155 160

ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc 528  
 Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu  
 165 170 175

gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac 576  
 Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His  
 180 185 190

aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc 624  
 Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys  
 195 200 205

tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag 672  
 Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys  
 210 215 220

ggg ggc cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg 720  
 Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu  
 225 230 235 240

gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc 768  
 Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile  
 245 250 255

ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc 816  
 Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg  
 260 265 270

ctc gtc ctc cgg tgc tcc atg 837  
 Leu Val Leu Arg Cys Ser Met  
 275

<210> 3

<211> 237

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (237)

<223> Coding sequence of the mature surfactant protein B

<400> 3

ttc ccc att cct ctc ccc tat tgc tgg ctc tgc agg gct ctg atc aag 48  
 Phe Pro Ile Pro Leu Pro Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys  
 1 5 10 15

cgg atc caa gcc atg att ccc aag ggt gcg cta gct gtg gca gtg gcc 96  
 Arg Ile Gln Ala Met Ile Pro Lys Gly Ala Leu Ala Val Ala Val Ala  
 20 25 30



cag	gtg	tgc	cgc	gtg	gta	cct	ctg	gtg	gcg	ggc	ggc	atc	tgc	cag	tgc	144	
Gln	Val	Cys	Arg	Val	Val	Pro	Leu	Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys		
35							40			45							
ctg	gct	gag	cgc	tac	tcc	gtc	atc	ctg	ctc	gac	acg	ctg	ctg	ggc	cgc	192	
Leu	Ala	Glu	Arg	Tyr	Ser	Val	Ile	Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg		
50							55			60							
atg	ctg	ccc	cag	ctg	gtc	tgc	cgc	ctc	gtc	ctc	cgg	tgc	tcc	atg		237	
Met	Leu	Pro	Gln	Leu	Val	Cys	Arg	Leu	Val	Leu	Arg	Cys	Ser	Met			
65							70			75							
<210> 4																	
<211> 1293																	
<212> DNA																	
<213> Homo sapiens																	
<220>																	
<221> CDS																	
<222> (1) ... (1293)																	
<223> Coding sequence of the single-chain urokinase-plasminogen acti																	
<400> 4																	
atg	aga	gcc	ctg	ctg	gcg	cgc	ctg	ctt	ctc	tgc	gtc	ctg	gtc	gtg	agc	48	
Met	Arg	Ala	Leu	Leu	Ala	Arg	Leu	Leu	Leu	Cys	Val	Leu	Val	Val	Ser		
1							5			10				15			
gac	tcc	aaa	ggc	agc	aat	gaa	ctt	cat	caa	gtt	cca	tcg	aac	tgt	gac	96	
Asp	Ser	Lys	Gly	Ser	Asn	Glu	Leu	His	Gln	Val	Pro	Ser	Asn	Cys	Asp		
			20								25				30		
tgt	cta	aat	gga	gga	aca	tgt	gtg	tcc	aac	aag	tac	ttc	tcc	aac	att	144	
Cys	Leu	Asn	Gly	Gly	Thr	Cys	Val	Ser	Asn	Lys	Tyr	Phe	Ser	Asn	Ile		
35							40			45							
cac	tgg	tgc	aac	tgc	cca	aag	aaa	ttc	gga	ggg	cag	cac	tgt	gaa	ata	192	
His	Trp	Cys	Asn	Cys	Pro	Lys	Lys	Phe	Gly	Gly	Gln	His	Cys	Glu	Ile		
50							55			60							
gat	aag	tca	aaa	acc	tgc	tat	gag	ggg	aat	ggt	cac	ttt	tac	cga	gga	240	
Asp	Lys	Ser	Lys	Thr	Cys	Tyr	Glu	Gly	Asn	Gly	His	Phe	Tyr	Arg	Gly		
65							70			75				80			
aag	gcc	agc	act	gac	acc	atg	ggc	cgg	ccc	tgc	ctg	ccc	tgg	aac	tct	288	
Lys	Ala	Ser	Thr	Asp	Thr	Met	Gly	Arg	Pro	Cys	Leu	Pro	Trp	Asn	Ser		
			85								90				95		
gcc	act	gtc	ctt	cag	caa	acg	tac	cat	gcc	cac	aga	tct	gat	gct	ctt	336	
Ala	Thr	Val	Leu	Gln	Gln	Thr	Tyr	His	Ala	His	Arg	Ser	Asp	Ala	Leu		
			100								105				110		
cag	ctg	ggc	ctg	ggg	aaa	cat	aat	tac	tgc	agg	aac	cca	gac	aac	cgg	384	
Gln	Leu	Gly	Leu	Gly	Lys	His	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Asn	Arg		
115							120			125							

agg cga ccc tgg tgc tat gtg cag gtg ggc cta aag ccg ctt gtc caa 432  
Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln  
130 135 140

gag tgc atg gtg cat gac tgc gca gat gga aaa aag ccc tcc tct cct 480  
Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro  
145 150 155 160

cca gaa gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc 528  
Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg  
165 170 175

ttt aag att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg 576  
Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp  
180 185 190

ttt gcg gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg 624  
Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val  
195 200 205

tgt gga ggc agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac 672  
Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His  
210 215 220

tgc ttc att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt 720  
Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly  
225 230 235 240

cgc tca agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg 768  
Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val  
245 250 255

gaa aac ctc atc cta cac aag gac tac agc gct gac acg ctt gct cac 816  
Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His  
260 265 270

cac aac gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt 864  
His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys  
275 280 285

gcg cag cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat 912  
Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr  
290 295 300

aac gat ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa 960  
Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys  
305 310 315 320

gag aat tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt 1008  
Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val  
325 330 335

gtg aag ctg att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc 1056  
Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly  
340 345 350

tct gaa gtc acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa 1104

Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys  
 355 360 365

aca gat tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc 1152  
 Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu  
 370 375 380

caa ggc cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt 1200  
 Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys  
 385 390 395 400

gcc ctg aag gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta 1248  
 Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu  
 405 410 415

ccc tgg atc cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc 1293  
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 420 425 430

<210> 5

<211> 828

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (828)

<223> Coding sequence of low mw two-chain urokinase-plasminogen activator

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 Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys  
 1 5 10 15

act ctg agg ccc cgc ttt aag att att ggg gga gaa ttc acc acc atc 96  
 Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile  
 20 25 30

gag aac cag ccc tgg ttt gcg gcc atc tac agg agg cac cgg ggg ggc 144  
 Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly  
 35 40 45

tct gtc acc tac gtg tgt gga ggc agc ctc atc agc cct tgc tgg gtg 192  
 Ser Val Thr Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val  
 50 55 60

atc agc gcc aca cac tgc ttc att gat tac cca aag aag gag gac tac 240  
 Ile Ser Ala Thr His Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr  
 65 70 75 80

atc gtc tac ctg ggt cgc tca agg ctt aac tcc aac acg caa ggg gag 288  
 Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu  
 85 90 95

atg aag ttt gag gtg gaa aac ctc atc cta cac aag gac tac agc gct	336
Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala	
100 105 110	
 gac acg ctt gct cac cac aac gac att gcc ttg ctg aag atc cgt tcc	384
Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser	
115 120 125	
 aag gag ggc agg tgt gcg cag cca tcc cgg act ata cag acc atc tgc	432
Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys	
130 135 140	
 ctg ccc tcg atg tat aac gat ccc cag ttt ggc aca agc tgt gag atc	480
Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile	
145 150 155 160	
 act ggc ttt gga aaa gag aat tct acc gac tat ctc tat ccg gag cag	528
Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln	
165 170 175	
 ctg aaa atg act gtt gtg aag ctg att tcc cac cgg gag tgt cag cag	576
Leu Lys Met Thr Val Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln	
180 185 1	